RAW SEQUENCE LISTING

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Application Serial Number: _____ 10/698,070A _____
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RAW SEQUENCE LISTING   DATE: 01/31/2006
PATENT APPLICATION: US/10/698,070A   TIME: 11:02:30

Input Set : **A:\221749.ST25.txt**
Output Set: **N:\CRF4\01312006\J698070A.raw**

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  3 <110> APPLICANT: GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY
  4        THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
  5        KAYE, FREDERIC J.
  6        KOMIYA, TAKEFUMI
  8 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A
CHIMERIC
  9        GENE
 11 <130> FILE REFERENCE: 221749
 13 <140> CURRENT APPLICATION NUMBER: 10/698,070A
 14 <141> CURRENT FILING DATE: 2003-10-30
 16 <160> NUMBER OF SEQ ID NOS: 12
 18 <170> SOFTWARE: PatentIn version 3.3
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 3763
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <400> SEQUENCE: 1
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 30 gagcctgacg cgggccgcgc ggctccaggg ttccttgaaa agaaaacagg tagttaacct     180
 32 atctcctgcc aacagcaagc gacccaatgg ctttgtggac aactcatttc ttgatatcaa     240
 34 aagaattcgt gttggggaga atctctctgc aggacaaggt ggcctccaaa taaacaatgg     300
 36 acaaagtcag attatgtcag ggaccttgcc tatgagccaa gcacccctgc gaaagactaa     360
 38 cactctgcca tcccatacac attctcctgg caatggcctg tttaacatgg gcttaaagga     420
 40 ggtaaagaag gagccaggag agactctgtc ttgcagtaag cacatggatg gccaaatgac     480
 42 ccaagagaat atttttccta ataggtacgg agacgaccct ggagaacaac tgatggatcc     540
 44 tgagctgcag gaactgttca atgaactgac caacatatct gtgcctccca tgagtgacct     600
 46 tgaactggag aacatgatca atgccaccat aaagcaggat gacccattta cattgactt      660
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 50 caaaagtgaa tactcaccgg gcttgactca gggcccctca ggctctcctc agctgaggcc     780
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 62 ttttggtcag cagacattca gcccacagag ctcccccatg cctggggtag ctggcggcag    1140
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 66 gcacctagat gtcctcatgc agcaaaagcc tcaggatctc agtcgaagtt ttattaacaa    1260
 68 cccgcaccca gccatggagc cccgtcaggg caacaccaag cctttgtttc attttaactc    1320
 70 agatcaagcg aaccagcaga tgccttctgt tttgccttcc cagaacaagc cttctctcct    1380
 72 acactacacc caacagcaac agcagcaaca gcagcagcag cagcagcagc agcagcagca    1440
 74 acagcagcag cagcagcaac agcaacagca acagcaacag cagagttcaa tttcagctca    1500
 76 acaacagcaa cagcagcaga gctcaatttc agcccaacag cagcagcagc agcaacaaca    1560
 78 gcagcagcag cagcaacaac aacagcaaca acagcagcag cagcagcagc aacaaccatc    1620
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 86 aagtcctaac ccctgctcaa atccaaacac tggaagtggt tacatgaact cccagcaatc   1860
 88 actgttgaat cagcaattga tgggaaagaa gcagactcta cagaggcaga tcatggagca   1920
 90 gaaacagcaa cttcttctcc agcagcagat gctggctgac gcggagaaaa ttgctccaca   1980
 92 agatcagata aaccgacatt tgtcaaggcc acctccagat tataaagacc aaagaagaaa   2040
 94 tgtgggcaat atgcaaccaa ctgctcagta ttctggtggc tcatccacaa taagcttaaa   2100
 96 ctctaaccag gctttggcaa acccagtttc aacacacacc attttaactc ccaattccag   2160
 98 cctcctgtct acttctcacg ggacaagaat gccatcatta tctacagcag ttcagaatat   2220
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102 gaatcaattg acccaacaga gaaacccaaa gcaattgtta gcaaatcaaa acaaccctat   2340
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106 tggatctgtt ggtaattcac aacaattgag accaaattta acccatagta tggcaagcat   2460
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112 cacaggtaca cctgcagcct ataccccaaa tcagtcactg caacaggcag taggtagcca   2640
114 gcaattttcc cagagggcag tggctcctcc taaccagtta acaccagcag tgcaaatgag   2700
116 acccatgaac caaatgagcc aaacactaaa tgggcaaacc atgggtcccc tcaggggtct   2760
118 gaatctcaga cccaatcagc taagcacaca gattttgcct aatttgaatc agtcaggaac   2820
120 agggttgaat cagtcgagga cgggcatcaa ccagccacca tccctgacgc ccagcaattt   2880
122 tccttcaccc aaccaaagtt ccagggcttt tcaaggaact gaccacagca gtgacttagc   2940
124 ttttgacttc ctcagccaac aaaatgataa catgggccct gccctaaaca gtgatgctga   3000
126 tttcattgat tctttattga agacagagcc tggtaatgat gactggatga aagacatcaa   3060
128 tcttgatgaa atcttgggga acaattccta aagaagaaag ggaagacaat ttacaaactc   3120
130 caagcactaa aaggcagtat attacagaaa ctctgtagag gctgaactgt tgatgttcag   3180
132 gtggactaca tgaagataac atgcttaaaa atggaaagca gaaagtaact gcagtgatga   3240
134 acattttggt ccaaattctt gttttaaatc ttacacctga aagtaaaata ttgggatcac   3300
136 ttttccctgt ctaaactcca ggatacagta tccaatttat ccaaacagaa ctgtggtgtc   3360
138 aatgtgtaat taattgtgta aaatagcctt cccaagtttc tttttccctg gaaaataaaa   3420
140 aaggtaatag aacttgtagt ttatttaaac cccatgtcat gaggaggtac tagttccaag   3480
142 caacaaactc cttaatttgc tctaatagat aggtatggtt taatctttcc attgtgtctt   3540
144 ttcatttaat tttcctgaag cttgcaggat agattgaaat gttataggtt tgtttggagt   3600
146 aaccaaacag tatgcaaatt aagaaaaagc cagagaacct agaaacatc cagtggatta    3660
148 cagaatttct tccccatatt cactcctcac ttttacaatt ttcccacaat cctctacttc   3720
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154 <211> LENGTH: 73
155 <212> TYPE: DNA
156 <213> ORGANISM: Unknown
158 <220> FEATURE:
159 <223> OTHER INFORMATION: RNAi clone
161 <400> SEQUENCE: 2
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164 ctaacagttt ttt                                                        73
167 <210> SEQ ID NO: 3
168 <211> LENGTH: 71
169 <212> TYPE: DNA
170 <213> ORGANISM: Unknown
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RAW SEQUENCE LISTING   DATE: 01/31/2006
PATENT APPLICATION: US/10/698,070A   TIME: 11:02:30

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172 <220> FEATURE:
173 <223> OTHER INFORMATION: RNAi clone
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178 gatcagtttt t                                                             71
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182 <211> LENGTH: 78
183 <212> TYPE: DNA
184 <213> ORGANISM: Unknown
186 <220> FEATURE:
187 <223> OTHER INFORMATION: RNAi clone - antisense
189 <400> SEQUENCE: 4
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192 gatcgcgctg cacaatcg                                                      78
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 28
197 <212> TYPE: DNA
198 <213> ORGANISM: Unknown
200 <220> FEATURE:
201 <223> OTHER INFORMATION: fragment of Mect1-MAML2 sequence
203 <400> SEQUENCE: 5
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207 <210> SEQ ID NO: 6
208 <211> LENGTH: 28
209 <212> TYPE: DNA
210 <213> ORGANISM: Unknown
212 <220> FEATURE:
213 <223> OTHER INFORMATION: fragment of Mect1-MAML2 sequence
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219 <210> SEQ ID NO: 7
220 <211> LENGTH: 28
221 <212> TYPE: DNA
222 <213> ORGANISM: Unknown
224 <220> FEATURE:
225 <223> OTHER INFORMATION: fragment of Mect1-MAML2 sequence
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231 <210> SEQ ID NO: 8
232 <211> LENGTH: 19
233 <212> TYPE: RNA
234 <213> ORGANISM: Unknown
236 <220> FEATURE:
237 <223> OTHER INFORMATION: siRNA #1
239 <400> SEQUENCE: 8
240 ccuaucuccu gccaacagc                                                     19
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 19
245 <212> TYPE: RNA
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246 <213> ORGANISM: Unknown
248 <220> FEATURE:
249 <223> OTHER INFORMATION: complement to siRNA #1
251 <400> SEQUENCE: 9
252 gcuguuggca ggagauagg                                          19
255 <210> SEQ ID NO: 10
256 <211> LENGTH: 19
257 <212> TYPE: RNA
258 <213> ORGANISM: Unknown
260 <220> FEATURE:
261 <223> OTHER INFORMATION: siRNA #2
263 <400> SEQUENCE: 10
264 cagguaguua accuaucuc                                          19
267 <210> SEQ ID NO: 11
268 <211> LENGTH: 19
269 <212> TYPE: RNA
270 <213> ORGANISM: Unknown
272 <220> FEATURE:
273 <223> OTHER INFORMATION: complement to siRNA #2
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276 gagauagguu aacuaccug                                          19
279 <210> SEQ ID NO: 12
280 <211> LENGTH: 1024
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <400> SEQUENCE: 12
286 Met Ala Thr Ser Asn Asn Pro Arg Lys Phe Ser Glu Lys Ile Ala Leu
287 1               5                   10                  15
290 His Asn Gln Lys Gln Ala Glu Glu Thr Ala Ala Phe Glu Glu Val Met
291             20                  25                  30
294 Lys Asp Leu Ser Leu Thr Arg Ala Ala Arg Leu Gln Gly Ser Leu Lys
295         35                  40                  45
298 Arg Lys Gln Val Val Asn Leu Ser Pro Ala Asn Ser Lys Arg Pro Asn
299     50                  55                  60
302 Gly Phe Val Asp Asn Ser Phe Leu Asp Ile Lys Arg Ile Arg Val Gly
303 65                  70                  75                  80
306 Glu Asn Leu Ser Ala Gly Gln Gly Gly Leu Gln Ile Asn Asn Gly Gln
307             85                  90                  95
310 Ser Gln Ile Met Ser Gly Thr Leu Pro Met Ser Gln Ala Pro Leu Arg
311             100                 105                 110
314 Lys Thr Asn Thr Leu Pro Ser His Thr His Ser Pro Gly Asn Gly Leu
315         115                 120                 125
318 Phe Asn Met Gly Leu Lys Glu Val Lys Lys Glu Pro Gly Glu Thr Leu
319     130                 135                 140
322 Ser Cys Ser Lys His Met Asp Gly Gln Met Thr Gln Glu Asn Ile Phe
323 145                 150                 155                 160
326 Pro Asn Arg Tyr Gly Asp Asp Pro Gly Glu Gln Leu Met Asp Pro Glu
327             165                 170                 175
330 Leu Gln Glu Leu Phe Asn Glu Leu Thr Asn Ile Ser Val Pro Pro Met
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RAW SEQUENCE LISTING   DATE: 01/31/2006
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331              180              185              190
334 Ser Asp Leu Glu Leu Glu Asn Met Ile Asn Ala Thr Ile Lys Gln Asp
335          195              200              205
338 Asp Pro Phe Asn Ile Asp Leu Gly Gln Gln Ser Gln Arg Ser Thr Pro
339          210              215              220
342 Arg Pro Ser Leu Pro Met Glu Lys Ile Val Ile Lys Ser Glu Tyr Ser
343 225              230              235              240
346 Pro Gly Leu Thr Gln Gly Pro Ser Gly Ser Pro Gln Leu Arg Pro Pro
347              245              250              255
350 Ser Ala Gly Pro Ala Phe Ser Met Ala Asn Ser Ala Leu Ser Thr Ser
351              260              265              270
354 Ser Pro Ile Pro Ser Val Pro Gln Ser Gln Ala Gln Pro Gln Thr Gly
355          275              280              285
358 Ser Gly Ala Ser Arg Ala Leu Pro Ser Trp Gln Glu Val Ser His Ala
359          290              295              300
362 Gln Gln Leu Lys Gln Ile Ala Ala Asn Arg Gln Gln His Ala Arg Met
363 305              310              315              320
366 Gln Gln His Gln Gln Gln His Gln Pro Thr Asn Trp Ser Ala Leu Pro
367              325              330              335
370 Ser Ser Ala Gly Pro Ser Pro Gly Pro Phe Gly Gln Glu Lys Ile Pro
371          340              345              350
374 Ser Pro Ser Phe Gly Gln Gln Thr Phe Ser Pro Gln Ser Ser Pro Met
375          355              360              365
378 Pro Gly Val Ala Gly Gly Ser Gly Gln Ser Lys Val Met Ala Asn Tyr
379          370              375              380
382 Met Tyr Lys Ala Gly Pro Ser Ala Gln Gly Gly His Leu Asp Val Leu
383 385              390              395              400
386 Met Gln Gln Lys Pro Gln Asp Leu Ser Arg Ser Phe Ile Asn Asn Pro
387              405              410              415
390 His Pro Ala Met Glu Pro Arg Gln Gly Asn Thr Lys Pro Leu Phe His
391          420              425              430
394 Phe Asn Ser Asp Gln Ala Asn Gln Gln Met Pro Ser Val Leu Pro Ser
395          435              440              445
398 Gln Asn Lys Pro Ser Leu Leu His Tyr Thr Gln Gln Gln Gln Gln Gln
399          450              455              460
402 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
403 465              470              475              480
406 Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Ser Ile Ser Ala Gln Gln
407              485              490              495
410 Gln Gln Gln Gln Gln Ser Ser Ile Ser Ala Gln Gln Gln Gln Gln Gln
411          500              505              510
414 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
415          515              520              525
418 Gln Gln Gln Gln Gln Pro Ser Ser Gln Pro Ala Gln Ser Leu Pro Ser
419          530              535              540
422 Gln Pro Leu Leu Arg Ser Pro Leu Pro Leu Gln Gln Lys Leu Leu Leu
423 545              550              555              560
426 Gln Gln Met Gln Asn Gln Pro Ile Ala Gly Met Gly Tyr Gln Val Ser
427              565              570              575
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